

SEQUENCE LISTING

<110> Rosson, Reinhardt D.
Deng, Ming-de
Grund, Alan D.

<120> LINOLEATE ISOMERASE

<130> 3161-20-C1

<140> Not Yet Assigned

<141> 2000-04-28

<150> 60/141,798

<151> 1999-06-30

<160> 80

<170> PatentIn Ver. 2.1

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<211> 35

<212> PRT

<213> Lactobacillus reuteri

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<221> UNSURE

<222> (30)

<223> Xaa = any amino acid

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Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Xaa Gly Leu
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Ala Ser Leu
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<212> DNA

<213> Lactobacillus reuteri

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<221> unsure

<222> (1)..(29)

<223> n = a, c, g, or t

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29

<210> 3

<211> 27

<212> DNA

<213> Lactobacillus reuteri

<220>

<221> unsure
<222> (1)..(27)
<223> n = a, c, g, or t

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27

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1 5 10 15

cct gct ggc gtt gat aag aaa cac gcc tac ata gtc gga 87
Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly
20 25

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<212> PRT
<213> Lactobacillus reuteri

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1 5 10 15

Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly
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17

<210> 7
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17

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<212> DNA
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a atg tat tat tca aac ggg aat tat gaa gcc ttt gct cga cca aag aag 169
Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Arg Pro Lys Lys
1 5 10 15

cct gct ggc gtt gat aag aaa cat gcc tac att gtc ggt ggt ggt tta 217
Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Gly Gly Leu
20 25 30

gct ggt tta tcg gcc gcc gtg ttt tta att cgt gat gcc caa atg ccg 265
Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro
35 40 45

ggt gag aat atc cat att tta gag gaa tta ccg gtt gcc ggt ggt tct 313
Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser
50 55 60

ctt gat ggt gaa gat cgt cct gga att ggt ttt gtt act cgt gga ggc 361
Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly
65 70 75 80

cgg gaa atg gag aac cat ttc gag tgt atg tgg gac atg tat cgt tca 409
Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser
85 90 95

att cca tca ctt gaa atc cca ggt gct tcc tac ctt gat gaa tac tac 457
Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr
100 105 110

tgg tta gat aag gaa gat cca aac agt tct aat tgt cgt tta acc tat 505
Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr
115 120 125

aag cgg gga aat gaa gtt cca tcg gac ggt aaa tat ggt tta agt aaa 553
Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys
130 135 140

aag gca atc aaa gag ctg act aag cta att atg acc cct aaa g 596
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<210> 9
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<212> PRT
<213> Lactobacillus reuteri

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 ataaagttgt tgagttaacg gacaatgacc ttgtctttgt cacaaacggg tcaattacag 1620
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 <211> 324
 <212> PRT
 <213> Lactobacillus reuteri

<220>
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 <222> (315)
 <223> Xaa = any amino acid

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 35 40 45
 Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser
 50 55 60
 Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly
 65 70 75 80
 Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser
 85 90 95
 Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr
 100 105 110
 Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr
 115 120 125
 Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys
 130 135 140
 Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Glu Glu Lys
 145 150 155 160
 Leu Gly Arg Glu Thr Ile Gly Glu Tyr Phe Ser Asp Asp Phe Phe Glu
 165 170 175
 Ser Asn Phe Trp Ile Tyr Trp Ser Thr Met Phe Ala Phe Glu Arg Trp
 180 185 190
 His Ser Leu Ala Glu Met Arg Arg Tyr Met Met Arg Phe Ile His His
 195 200 205
 Ile Asp Gly Leu Pro Asp Phe Thr Ala Leu Lys Phe Asn Lys Tyr Asn
 210 215 220
 Gln Tyr Glu Ser Met Thr Lys Pro Leu Leu Ala Tyr Leu Lys Asp His
 225 230 235 240

His Val Lys Ile Glu Tyr Asp Thr Gln Val Lys Asn Val Ile Val Asp
245 250 255

Thr His Gly Arg Gln Lys His Ala Lys Arg Ile Leu Leu Thr Gln Ala
260 265 270

Gly Lys Asp Lys Val Val Glu Leu Thr Asp Asn Asp Leu Val Phe Val
275 280 285

Thr Asn Gly Ser Ile Thr Glu Ser Ser Thr Tyr Gly Ser His His Gln
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Ala Ser Ser Thr Asn Ala Ala Leu Gly Gly Xaa Leu Glu Thr Val Gly
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Lys Pro Cys Ser

<210> 12
<211> 17
<212> DNA
<213> Lactobacillus reuteri

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17

<210> 13
<211> 19
<212> DNA
<213> Lactobacillus reuteri

<400> 13
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19

<210> 14
<211> 1165
<212> DNA
<213> Lactobacillus reuteri

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gaggaattac cggttgaata attaatggta atgtttcttt ggacattcgg aacaaagaca 180
ttgtattcta gagaaccatc actagattta gcttcgatat gagcacctgc cggaacgata 240
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ataccacca actagtgc ataggcaagaa ggtgtccgcg atcgtatgca tgattgtacc 480
cgcctttaag attatgcgcc tgaaggaag ccagctggtc gccaatccgt agcaccattc 540
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ctaataattc caaagtctat tttactagtt tgaacatacg tttggaataa ttatttagaa 1020

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<210> 15
 <211> 2319
 <212> DNA
 <213> *Lactobacillus reuteri*

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 aagaagggct tcaatactgg cttaaaatcc tttttaaaagt ggtagtaag gttttggtat 180
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 gaagcttcgt ctaaactctac actcccaaga atcacacggg aatcatgagt agttgaacta 300
 cttaacaagt aaaacttaga atggataacc tgagtaggag cgattgatac gcgaaaaaga 360
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<210> 16
 <211> 3551
 <212> DNA
 <213> *Lactobacillus reuteri*

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 gtcataaata ttggtaactc ggtagcgaac ttgcttattc tgatctaag cttttctcac 180

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<212> DNA

<213> Lactobacillus reuteri

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<221> CDS

<222> (1)..(1776)

<400> 17

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Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Gly Gly Leu	
20 25 30	
gct ggt tta tcg gcc gcc gtg ttt tta att cgt gat gcc caa atg ccg	144
Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro	
35 40 45	
ggt gag aat atc cat att tta gag gaa tta ccg gtt gcc ggt ggt tct	192
Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser	
50 55 60	
ctt gat ggt gaa gat cgt cct gga att ggt ttt gtt act cgt gga ggc	240
Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly	
65 70 75 80	
cgg gaa atg gag aac cat ttc gag tgt atg tgg gac atg tat cgt tca	288
Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser	
85 90 95	
att cca tca ctt gaa atc cca ggt gct tcc tac ctt gat gaa tac tac	336
Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr	
100 105 110	
tgg tta gat aag gaa gat cca aac agt tct aat tgt cgt tta acc tat	384
Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr	
115 120 125	
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Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys	
130 135 140	
aag gca atc aaa gag ctg act aag cta att atg acc cct gaa gaa aaa	480
Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Glu Glu Lys	
145 150 155 160	
ttg gga agg gag act att ggt gaa tac ttc tct gat gat ttc ttt gaa	528
Leu Gly Arg Glu Thr Ile Gly Glu Tyr Phe Ser Asp Asp Phe Phe Glu	
165 170 175	
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Ser Asn Phe Trp Ile Tyr Trp Ser Thr Met Phe Ala Phe Glu Arg Trp	
180 185 190	
cac tct cta gct gaa atg cgt cgt tat atg atg cgg ttt att cac cat	624
His Ser Leu Ala Glu Met Arg Arg Tyr Met Met Arg Phe Ile His His	
195 200 205	
att gat ggt tta ccg gat ttc act gca ctg aag ttt aat aag tat aac	672

Ile Asp Gly Leu Pro Asp Phe Thr Ala Leu Lys Phe Asn Lys Tyr Asn 210 215 220	
caa tat gaa tca atg acc aag ccg cta ttg gcc tac ctg aaa gat cat Gln Tyr Glu Ser Met Thr Lys Pro Leu Leu Ala Tyr Leu Lys Asp His 225 230 235 240	720
cat gtc aag att gag tac gat acc cag gta aag aat gtt att gtt gat His Val Lys Ile Glu Tyr Asp Thr Gln Val Lys Asn Val Ile Val Asp 245 250 255	768
act cat ggg cgg caa aag cac gct aag cga atc tta tta act caa gcc Thr His Gly Arg Gln Lys His Ala Lys Arg Ile Leu Leu Thr Gln Ala 260 265 270	816
ggt aaa gat aaa gtt gtt gag tta acg gac aat gac ctt gtc ttt gtc Gly Lys Asp Lys Val Val Glu Leu Thr Asp Asn Asp Leu Val Phe Val 275 280 285	864
aca aac ggt tca att aca gaa agt tct act tac ggc agt cac cat caa Thr Asn Gly Ser Ile Thr Glu Ser Ser Thr Tyr Gly Ser His His Gln 290 295 300	912
gca gct cga cca acg caa gca ctt ggt ggt agt tgg aaa ctg tgg gaa Ala Ala Arg Pro Thr Gln Ala Leu Gly Gly Ser Trp Lys Leu Trp Glu 305 310 315 320	960
aac ctt gct cgg cag tca gct gat ttt ggt cat cct gat gtc ttt tgc Asn Leu Ala Arg Gln Ser Ala Asp Phe Gly His Pro Asp Val Phe Cys 325 330 335	1008
aag aat ctt cca ggg aga agc tgg ttc att tcc gct act gca acc gtt Lys Asn Leu Pro Gly Arg Ser Trp Phe Ile Ser Ala Thr Ala Thr Val 340 345 350	1056
aag aac ccg caa gtt gaa cca tac att gaa cgc tta acc aag cga gat Lys Asn Pro Gln Val Glu Pro Tyr Ile Glu Arg Leu Thr Lys Arg Asp 355 360 365	1104
ctc cat gat ggc aaa gtt aat act ggt gga atc att acg gtc act gac Leu His Asp Gly Lys Val Asn Thr Gly Gly Ile Ile Thr Val Thr Asp 370 375 380	1152
tct aat tgg atg ctt tcc tgg aca att cac cgt caa ccg cac ttc aag Ser Asn Trp Met Leu Ser Trp Thr Ile His Arg Gln Pro His Phe Lys 385 390 395 400	1200
aaa caa aag aaa aat gaa acc att gtt tgg att tac ggt ctg tac tct Lys Gln Lys Lys Asn Glu Thr Ile Val Trp Ile Tyr Gly Leu Tyr Ser 405 410 415	1248
aat aca aag gga aac tat att aag aaa cgg atc gtt gat tgt act ggt Asn Thr Lys Gly Asn Tyr Ile Lys Lys Arg Ile Val Asp Cys Thr Gly 420 425 430	1296
gaa gag att act aaa gaa tgg cta tcc atc tgg ggg ttc cag aag ccg Glu Glu Ile Thr Lys Glu Trp Leu Ser Ile Trp Gly Phe Gln Lys Pro 435 440 445	1344
tta att gac gat ttg gct aag gag agt tca att aat act gtt cca gta Leu Ile Asp Asp Leu Ala Lys Glu Ser Ser Ile Asn Thr Val Pro Val	1392

450	455	460	
tat atg cca ttt atc act agc tac ttt atg cca cga gtt aag ggc gac			1440
Tyr Met Pro Phe Ile Thr Ser Tyr Phe Met Pro Arg Val Lys Gly Asp			
465	470	475	480
cgt cca gac gtt gtt cca gaa gga tcc gct aac ttg gca ttt att ggt			1488
Arg Pro Asp Val Val Pro Glu Gly Ser Ala Asn Leu Ala Phe Ile Gly			
	485	490	495
aac ttt gct gaa tct cca agt cga gat acc gta ttt acc acg gaa tat			1536
Asn Phe Ala Glu Ser Pro Ser Arg Asp Thr Val Phe Thr Thr Glu Tyr			
	500	505	510
tca gta cgg acc gca atg gaa gcc gtc tac act cta tta gat gtt gat			1584
Ser Val Arg Thr Ala Met Glu Ala Val Tyr Thr Leu Leu Asp Val Asp			
	515	520	525
cgg gga gtt cca gaa gtc ttt aac tct att tat gat ctt cga gag tta			1632
Arg Gly Val Pro Glu Val Phe Asn Ser Ile Tyr Asp Leu Arg Glu Leu			
	530	535	540
atg cgg gca atg tat tac atg aat gat aag aag ccg tta aaa gac atg			1680
Met Arg Ala Met Tyr Tyr Met Asn Asp Lys Lys Pro Leu Lys Asp Met			
545	550	555	560
gac ttg cca att cca aag att gtt gaa aag cca tta tta aag aaa ctc			1728
Asp Leu Pro Ile Pro Lys Ile Val Glu Lys Pro Leu Leu Lys Lys Leu			
	565	570	575
caa gga acg tgg att ggt gaa tta atg gag caa cag cac tta cta taa			1776
Gln Gly Thr Trp Ile Gly Glu Leu Met Glu Gln Gln His Leu Leu			
	580	585	590

<210> 18
 <211> 591
 <212> PRT
 <213> Lactobacillus reuteri

<400> 18
Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Arg Pro Lys Lys
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Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Gly Leu
20 25 30
Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro
35 40 45
Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser
50 55 60
Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly
65 70 75 80
Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser
85 90 95
Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr
100 105 110
Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr
115 120 125
Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys
130 135 140
Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Glu Glu Lys
145 150 155 160

Leu	Gly	Arg	Glu	Thr	Ile	Gly	Glu	Tyr	Phe	Ser	Asp	Asp	Phe	Phe	Glu			
				165					170						175			
Ser	Asn	Phe	Trp	Ile	Tyr	Trp	Ser	Thr	Met	Phe	Ala	Phe	Glu	Arg	Trp			
			180					185					190					
His	Ser	Leu	Ala	Glu	Met	Arg	Arg	Tyr	Met	Met	Arg	Phe	Ile	His	His			
		195					200					205						
Ile	Asp	Gly	Leu	Pro	Asp	Phe	Thr	Ala	Leu	Lys	Phe	Asn	Lys	Tyr	Asn			
	210					215					220							
Gln	Tyr	Glu	Ser	Met	Thr	Lys	Pro	Leu	Leu	Ala	Tyr	Leu	Lys	Asp	His			
225					230					235					240			
His	Val	Lys	Ile	Glu	Tyr	Asp	Thr	Gln	Val	Lys	Asn	Val	Ile	Val	Asp			
				245				250						255				
Thr	His	Gly	Arg	Gln	Lys	His	Ala	Lys	Arg	Ile	Leu	Leu	Thr	Gln	Ala			
		260					265						270					
Gly	Lys	Asp	Lys	Val	Val	Glu	Leu	Thr	Asp	Asn	Asp	Leu	Val	Phe	Val			
	275					280					285							
Thr	Asn	Gly	Ser	Ile	Thr	Glu	Ser	Ser	Thr	Tyr	Gly	Ser	His	His	Gln			
	290				295					300								
Ala	Ala	Arg	Pro	Thr	Gln	Ala	Leu	Gly	Gly	Ser	Trp	Lys	Leu	Trp	Glu			
305					310				315						320			
Asn	Leu	Ala	Arg	Gln	Ser	Ala	Asp	Phe	Gly	His	Pro	Asp	Val	Phe	Cys			
				325				330						335				
Lys	Asn	Leu	Pro	Gly	Arg	Ser	Trp	Phe	Ile	Ser	Ala	Thr	Ala	Thr	Val			
		340					345						350					
Lys	Asn	Pro	Gln	Val	Glu	Pro	Tyr	Ile	Glu	Arg	Leu	Thr	Lys	Arg	Asp			
	355					360					365							
Leu	His	Asp	Gly	Lys	Val	Asn	Thr	Gly	Gly	Ile	Ile	Thr	Val	Thr	Asp			
	370				375					380								
Ser	Asn	Trp	Met	Leu	Ser	Trp	Thr	Ile	His	Arg	Gln	Pro	His	Phe	Lys			
385				390					395						400			
Lys	Gln	Lys	Lys	Asn	Glu	Thr	Ile	Val	Trp	Ile	Tyr	Gly	Leu	Tyr	Ser			
			405					410						415				
Asn	Thr	Lys	Gly	Asn	Tyr	Ile	Lys	Lys	Arg	Ile	Val	Asp	Cys	Thr	Gly			
		420					425						430					
Glu	Glu	Ile	Thr	Lys	Glu	Trp	Leu	Ser	Ile	Trp	Gly	Phe	Gln	Lys	Pro			
	435				440						445							
Leu	Ile	Asp	Asp	Leu	Ala	Lys	Glu	Ser	Ser	Ile	Asn	Thr	Val	Pro	Val			
	450				455					460								
Tyr	Met	Pro	Phe	Ile	Thr	Ser	Tyr	Phe	Met	Pro	Arg	Val	Lys	Gly	Asp			
465				470					475						480			
Arg	Pro	Asp	Val	Val	Pro	Glu	Gly	Ser	Ala	Asn	Leu	Ala	Phe	Ile	Gly			
			485					490						495				
Asn	Phe	Ala	Glu	Ser	Pro	Ser	Arg	Asp	Thr	Val	Phe	Thr	Thr	Glu	Tyr			
		500					505						510					
Ser	Val	Arg	Thr	Ala	Met	Glu	Ala	Val	Tyr	Thr	Leu	Leu	Asp	Val	Asp			
	515					520						525						
Arg	Gly	Val	Pro	Glu	Val	Phe	Asn	Ser	Ile	Tyr	Asp	Leu	Arg	Glu	Leu			
	530				535					540								
Met	Arg	Ala	Met	Tyr	Tyr	Met	Asn	Asp	Lys	Lys	Pro	Leu	Lys	Asp	Met			
545				550					555						560			
Asp	Leu	Pro	Ile	Pro	Lys	Ile	Val	Glu	Lys	Pro	Leu	Leu	Lys	Lys	Leu			
			565				570							575				
Gln	Gly	Thr	Trp	Ile	Gly	Glu	Leu	Met	Glu	Gln	Gln	His	Leu	Leu				
			580				585						590					

<210> 19

<211> 656

<212> DNA

<213> Lactobacillus reuteri

<220>
 <221> CDS
 <222> (1)..(654)

<400> 19

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Met Val Met Thr Glu Thr Ala Gly Ile Arg Lys Ile His Ile Val Phe	
1 5 10 15	
gat ggt caa gaa aca cca cca tta aag atc cat caa tta ttt gat tca	96
Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser	
20 25 30	
caa aaa tac gat cag tta atc gca gta act ggg aaa att act gct gac	144
Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp	
35 40 45	
ttc att aat aaa tac ctt agt aat ttt atc agt att aat gta gcg tta	192
Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu	
50 55 60	
agc tcc caa tca act agt gaa tta agt gct gat gag atg gtg aca aag	240
Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys	
65 70 75 80	
gtt gca ctt acc aat gct ctc ctt agt tca gca aat aaa gaa gct gct	288
Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala	
85 90 95	
aaa ctc ttc tca gcg tta acc agt gac aac caa acg aac gtc tta aat	336
Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn	
100 105 110	
aat ctt ttt cgc gta tca atc gcg cct act cag gtt atc cat tct aag	384
Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys	
115 120 125	
ttt tac ttg tta agt agt tca act act cat gat tcc cgt gtg att ctt	432
Phe Tyr Leu Leu Ser Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu	
130 135 140	
ggg agt gta gat tta gac gaa gct tca ttt gat gct cac cga aat caa	480
Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln	
145 150 155 160	
ttt gaa gaa gta ttg gta ttt gac aat gat gtc cgc tta tac caa aac	528
Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn	
165 170 175	
ctt act gac cac ttt aaa aag gat ttt aag cca gta ttg aag ccc ttc	576
Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe	
180 185 190	
ttt act atg aac cta gta aag gca gct caa aag caa gtt gag gaa gga	624
Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly	
195 200 205	
aag aaa gat cag gat agc ggt aag gga ccg gt	656
Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro	
210 215	

<210> 20
 <211> 218
 <212> PRT
 <213> Lactobacillus reuteri

<400> 20
 Met Val Met Thr Glu Thr Ala Gly Ile Arg Lys Ile His Ile Val Phe
 1 5 10 15
 Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser
 20 25 30
 Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp
 35 40 45
 Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu
 50 55 60
 Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys
 65 70 75 80
 Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala
 85 90 95
 Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn
 100 105 110
 Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys
 115 120 125
 Phe Tyr Leu Leu Ser Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu
 130 135 140
 Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln
 145 150 155 160
 Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn
 165 170 175
 Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe
 180 185 190
 Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly
 195 200 205
 Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro
 210 215

<210> 21
 <211> 726
 <212> DNA
 <213> Lactobacillus reuteri

<220>
 <221> CDS
 <222> (1)..(726)

<220>
 <221> unsure
 <222> (1)..(726)
 <223> n = a, c, g, or t

<400> 21

atg ctt cgt tan acc ata tta gta aaa ttg ctt att gga aga aaa cca	48
Met Leu Arg Xaa Thr Ile Leu Val Lys Leu Leu Ile Gly Arg Lys Pro	
1 5 10 15	
gtc aca acg atc aaa aaa aca tta ccg cca act cag gaa cag gct aat	96
Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn	
20 25 30	
tca gtc tta act ccg gct gtt cgc caa caa ctt ggc att tca att acc	144
Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr	
35 40 45	
tgg aac aaa gcc ggt gcg ttt att atc aat aat aac caa aca aat ctt	192
Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu	
50 55 60	
aac gct aag att gca agt gca ccc tat gct gta aat cat ctt gac cgt	240
Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg	
65 70 75 80	
caa gga agg gcg tgg caa ggt gat gcc tgg tta aac agg aca act cgg	288
Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg	
85 90 95	
tca ata tan aag ccg aaa ttt gcc aca ggg aat ggt gct acg gat tgg	336
Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp	
100 105 110	
cga cca gct ggc ttc ctt cag gcg cat aat ctt aaa ggc ggg tac aat	384
Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn	
115 120 125	
cat gca tac gat cgc gga cac ctt ctt gcc tat gca cta gtt ggt ggt	432
His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly	
130 135 140	
att cat gga ttt gat gca tcc gaa tca aat cca tct aat att gcc acg	480
Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr	
145 150 155 160	
caa act gcc tgg gca aat gaa gca cga agt aag aac tca aca ggg caa	528
Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln	
165 170 175	
aat tac tac gaa ggt ctg gtg aga aaa gca tta gat cag aat aag caa	576
Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln	
180 185 190	
gtt cgc tac cga gtt acc aat att tat gac ggt aat aat atc gtt ccg	624
Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro	
195 200 205	
gca ggt gct cat atc gaa gct aaa tct agt gat ggt tct cta gaa tac	672
Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr	
210 215 220	

aat gtc ttt gtt ccg aat gtc caa aga aac att acc att aat tat tca 720
 Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser
 225 230 235 240

acc ggt 726
 Thr Gly

<210> 22
 <211> 242
 <212> PRT
 <213> Lactobacillus reuteri

<220>
 <221> UNSURE
 <222> (1)..(242)
 <223> Xaa = Tyr or stop

<400> 22
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 1 5 10 15
 Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn
 20 25 30
 Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr
 35 40 45
 Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu
 50 55 60
 Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg
 65 70 75 80
 Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg
 85 90 95
 Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp
 100 105 110
 Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn
 115 120 125
 His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly
 130 135 140
 Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr
 145 150 155 160
 Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln
 165 170 175
 Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln
 180 185 190
 Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro
 195 200 205
 Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr
 210 215 220

Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser
 225 230 235 240

Thr Gly

<210> 23
 <211> 18
 <212> DNA
 <213> Lactobacillus reuteri

<400> 23
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<210> 24
 <211> 18
 <212> DNA
 <213> Lactobacillus reuteri

<400> 24
 caagttgagg aaggaaag 18

<210> 25
 <211> 3684
 <212> DNA
 <213> Lactobacillus reuteri

<400> 25
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 gaaacaacag ataagatcgc tgaaacagac atgggtggatc tgttgaagca tgaccttcag 120
 catgatattg accataatct tgttcctgaa atgatacaca agtcaatgcg tgatattacc 180
 ataaatcggt ctcaagcaaa ggagaaaatt gctaagcagg ttaagcaaca tgatacgatt 240
 tatactttgc aaaaagaagc ggtctctcct cgggcagcta agccaaaact aaagactcga 300
 gaaaaaatta ccaagcaggc tcaggatgct ttgatcagtg gaatgtcacc acagcaacgg 360
 gatgctgaga aaaagtacac gacttttctg tacgatcggc caatggaacg aaacattgcg 420
 aataacaata gtggcctata cgttcctaata gatacgggaa ctaccccaat cccatttggt 480
 aaaattgcaa ctatttctga aattcgtgac gggttaaaga gcattgatgc tggtatgaag 540
 ggctatcagc agtttgtcgt tgattatgat gctgactacg ggaagcgggt ctttgaagca 600
 attttgtata gttttactgc accgttttta tgggaaattc gttctaaagc tagcctgaac 660
 cctgaagatg ggaatgatgt tcctaatttc ctaatcctag gggcaacggc tggttccgga 720
 aagtctaccc ttcttcggat tattaatcag ctacagtgga acactgatcg ctcggttgatt 780
 gactttggaa cgatctaccc gtcgcaaaact cctcaaaaga aggcaaagac tgttgaggcg 840
 atggaacatt atatgaaact tggtagttca taccgggttt tgtagatga aattgaaccg 900
 tacttcttcc agcaagatca atatagtcga ctggagttct gggttgctat gattaagggtt 960
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 aactggcacc cagttgggat ttctaatttg tgggtctcatg gcggattctt taccgggtggc 1080
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 tccgttatct ggcggatctt aatcttctat attgggtgcaa ttttcgtcat tgtttctatt 1260
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 tggtttatca ttctcttgct agaacttcac ttcagaaaag aacaccctga acagcttaaa 1680

gatcatccat	tcaagatgcc	gctttaccgc	gcttataact	acttttagttt	gattgccttg	1740
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gttatcttct	tgattatcat	gagtattatt	tatcgtgttc	gtgttcatga	aggaaaagaa	1860
aagtaaatat	atagctaaag	cagctttgta	aatcctgcgt	acaatacccc	ttagggttga	1920
cactttaaat	aataaaagt	tgaatcctag	ggggtgtttt	gcattgtaag	ttattcaact	1980
attgaaaagc	ttaaattact	tcatgattat	cagaaatcgg	attatggttt	aacggtgtac	2040
tccgattacc	atggtgtccg	accagcaaac	atgagtaagt	ggattaagca	attcctactc	2100
gctggattgg	cgggattaat	tagacctaa	cataatcaga	agtactcatt	agagactaag	2160
ttactgctg	taaaagctta	tctttctggc	aagtatacta	atcaagcaat	tctccagcag	2220
tatcaaatta	gaaatatttc	tcaactacat	caatgggtta	tcagttacaa	taatgacaaa	2280
ctccgagtta	atcagacaac	gagaaagcga	gtcagaaaaa	tgggacgaaa	agtaaccttt	2340
gatgaaaaga	ggcagattgt	ccgatggaca	attgaacata	acaataacta	taaagcggct	2400
gcagagaagt	atgatattag	ttaccaacga	gtttattctt	gggtacggaa	gtaccgagta	2460
aatagcgact	gggaagtact	aaaagataac	cgtgggcgta	ataaaggaaa	agagcccact	2520
aatgaactag	aaaaactaag	gaaacgagtt	cgtgagctag	aagatcgtga	ccgtgaacgg	2580
gagctgcaaa	tcgctttcgc	aaaaaaatta	gtcgaaatac	gcaatcggga	ggtgaaacga	2640
ccggacgata	tcaagcgatt	caagaaatga	acaatgaagg	ttattccatt	agtgaattgg	2700
ccaaggctgc	tgggaattact	agacaggctt	actacaaatg	gttgaaacat	gaaccgacta	2760
aatatgagat	tgaagaatcg	gagattctcc	aattgattaa	acagttagaa	aatgaacata	2820
agcaaagcgt	tggttatgac	aaaatgacta	ggttaatcaa	gttaagtcag	cagatctctt	2880
ataccgttaa	taagaaacga	gtcattcgt	ttatgaaagg	ccatagtatc	aaggccgact	2940
atcgtcagcc	aaccgacaaa	cgtattcaag	cccagcaaac	ttatgaagct	gaaaatatct	3000
ttaaccgaca	atttgaccaa	actgcagcta	accaagtttg	ggttacggat	acgacggaac	3060
tgaattacgg	aatctggctt	aataaagttc	gtctacatat	agtattagat	ttatatggtc	3120
aatacccagt	aagctggtta	attacaccta	cagaaaccgc	tgaaggagta	gttcaagtgt	3180
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<210> 26

<211> 7113

<212> DNA

<213> *Lactobacillus reuteri*

<220>

<221> unsure

<222> (1)..(7113)

<223> n = a, c, g, or t

<400> 26

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<210> 27
 <211> 941
 <212> DNA
 <213> *Lactobacillus reuteri*

<220>
 <221> CDS
 <222> (3)..(941)

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 Arg Leu Glu Phe Trp Phe Ala Met Ile Lys Val Val Thr Ile Ile
 1 5 10 15

gca atg att att ctt ggt tta ctg gtt atc gtt ctt ggg tta ggt aat 95

Ala Met Ile Ile Leu Gly Leu Leu Val Ile Val Leu Gly Leu Gly Asn	
20 25 30	
aac tgg cac cca gtt ggg att tct aat ttg tgg tct cat ggc gga ttc	143
Asn Trp His Pro Val Gly Ile Ser Asn Leu Trp Ser His Gly Gly Phe	
35 40 45	
ttt acc ggt ggc ttt atg ggc ttt atg ttc tgc cta tct gtg att gct	191
Phe Thr Gly Gly Phe Met Gly Phe Met Phe Ser Leu Ser Val Ile Ala	
50 55 60	
ggt tct tat cag gga att gag tta ttg gga atc act gct ggt gaa gct	239
Gly Ser Tyr Gln Gly Ile Glu Leu Leu Gly Ile Thr Ala Gly Glu Ala	
65 70 75	
gaa tca cca cgt cat gcg att gtg aaa tca gtt aag tcc gtt atc tgg	287
Glu Ser Pro Arg His Ala Ile Val Lys Ser Val Lys Ser Val Ile Trp	
80 85 90 95	
cgg atc tta atc ttc tat att ggt gca att ttc gtc att gtt tct att	335
Arg Ile Leu Ile Phe Tyr Ile Gly Ala Ile Phe Val Ile Val Ser Ile	
100 105 110	
tac cca tgg aac gaa ttg aag tcc gtt ggc tca cca ttc gtt gaa acc	383
Tyr Pro Trp Asn Glu Leu Lys Ser Val Gly Ser Pro Phe Val Glu Thr	
115 120 125	
ttc acg aag gtt gga att act gga gca gcc gga atc att aac ttt gtt	431
Phe Thr Lys Val Gly Ile Thr Gly Ala Ala Gly Ile Ile Asn Phe Val	
130 135 140	
gtt ttg acg gca gct ctt tct gga gct aac tct gga att tac agt gct	479
Val Leu Thr Ala Ala Leu Ser Gly Ala Asn Ser Gly Ile Tyr Ser Ala	
145 150 155	
agt cgg atg ttg ttc aag ctt tct gtt gat ggg gaa gta cca aag ttc	527
Ser Arg Met Leu Phe Lys Leu Ser Val Asp Gly Glu Val Pro Lys Phe	
160 165 170 175	
ttt agt aag ctt tcc aag cgc gtt gtt cct aat gtt gca atc ctc acg	575
Phe Ser Lys Leu Ser Lys Arg Val Val Pro Asn Val Ala Ile Leu Thr	
180 185 190	
att tct tcc tgg atc ttc ctt ggc ttt gta att aat gaa tta atg tgc	623
Ile Ser Ser Trp Ile Phe Leu Gly Phe Val Ile Asn Glu Leu Met Ser	
195 200 205	
att ttt agt tct gct gct caa aat att ttc gtc att gta tat agt tcc	671
Ile Phe Ser Ser Ala Ala Gln Asn Ile Phe Val Ile Val Tyr Ser Ser	
210 215 220	
agt gtt ctt cca ggg atg gta cca tgg ttt atc att ctc ttg tca gaa	719
Ser Val Leu Pro Gly Met Val Pro Trp Phe Ile Ile Leu Leu Ser Glu	
225 230 235	
ctt cac ttc aga aaa gaa cac cct gaa cag ctt aaa gat cat cca ttc	767
Leu His Phe Arg Lys Glu His Pro Glu Gln Leu Lys Asp His Pro Phe	
240 245 250 255	
aag atg ccg ctt tac ccg gct tat aac tac ttt agt ttg att gcc ttg	815
Lys Met Pro Leu Tyr Pro Ala Tyr Asn Tyr Phe Ser Leu Ile Ala Leu	

	260	265	270	
act gtg atc ttg atc ttc atg ttc ttt aac cca gat act cga gtt tca				863
Thr Val Ile Leu Ile Phe Met Phe Phe Asn Pro Asp Thr Arg Val Ser				
	275	280	285	
gta tca gtt ggt gtt atc ttc ttg att atc atg agt att att tat cgt				911
Val Ser Val Gly Val Ile Phe Leu Ile Ile Met Ser Ile Ile Tyr Arg				
	290	295	300	
gtt cgt gtt cat gaa gga aaa gaa aag taa				941
Val Arg Val His Glu Gly Lys Glu Lys				
	305	310		

<210> 28
 <211> 312
 <212> PRT
 <213> *Lactobacillus reuteri*

<400> 28

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Met Ile Ile Leu Gly Leu Leu Val Ile Val Leu Gly Leu Gly Asn Asn				
20 25 30				
Trp His Pro Val Gly Ile Ser Asn Leu Trp Ser His Gly Gly Phe Phe				
35 40 45				
Thr Gly Gly Phe Met Gly Phe Met Phe Ser Leu Ser Val Ile Ala Gly				
50 55 60				
Ser Tyr Gln Gly Ile Glu Leu Leu Gly Ile Thr Ala Gly Glu Ala Glu				
65 70 75 80				
Ser Pro Arg His Ala Ile Val Lys Ser Val Lys Ser Val Ile Trp Arg				
85 90 95				
Ile Leu Ile Phe Tyr Ile Gly Ala Ile Phe Val Ile Val Ser Ile Tyr				
100 105 110				
Pro Trp Asn Glu Leu Lys Ser Val Gly Ser Pro Phe Val Glu Thr Phe				
115 120 125				
Thr Lys Val Gly Ile Thr Gly Ala Ala Gly Ile Ile Asn Phe Val Val				
130 135 140				
Leu Thr Ala Ala Leu Ser Gly Ala Asn Ser Gly Ile Tyr Ser Ala Ser				
145 150 155 160				
Arg Met Leu Phe Lys Leu Ser Val Asp Gly Glu Val Pro Lys Phe Phe				
165 170 175				
Ser Lys Leu Ser Lys Arg Val Val Pro Asn Val Ala Ile Leu Thr Ile				
180 185 190				
Ser Ser Trp Ile Phe Leu Gly Phe Val Ile Asn Glu Leu Met Ser Ile				
195 200 205				
Phe Ser Ser Ala Ala Gln Asn Ile Phe Val Ile Val Tyr Ser Ser Ser				
210 215 220				
Val Leu Pro Gly Met Val Pro Trp Phe Ile Ile Leu Leu Ser Glu Leu				
225 230 235 240				
His Phe Arg Lys Glu His Pro Glu Gln Leu Lys Asp His Pro Phe Lys				
245 250 255				
Met Pro Leu Tyr Pro Ala Tyr Asn Tyr Phe Ser Leu Ile Ala Leu Thr				
260 265 270				
Val Ile Leu Ile Phe Met Phe Phe Asn Pro Asp Thr Arg Val Ser Val				
275 280 285				
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Arg Val His Glu Gly Lys Glu Lys				
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<210> 29
 <211> 600
 <212> DNA
 <213> Lactobacillus reuteri

<220>
 <221> CDS
 <222> (1)..(597)

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 1 5 10 15
 att aga cct aag cat aat cag aag tac tca tta gag act aag tta act 96
 Ile Arg Pro Lys His Asn Gln Lys Tyr Ser Leu Glu Thr Lys Leu Thr
 20 25 30
 gct gta aaa gct tat ctt tct ggc aag tat act aat caa gca att ctc 144
 Ala Val Lys Ala Tyr Leu Ser Gly Lys Tyr Thr Asn Gln Ala Ile Leu
 35 40 45
 cag cag tat caa att aga aat att tct caa cta cat caa tgg gtt atc 192
 Gln Gln Tyr Gln Ile Arg Asn Ile Ser Gln Leu His Gln Trp Val Ile
 50 55 60
 agt tac aat aat gac aaa ctc cga gtt aat cag aca acg aga aag cga 240
 Ser Tyr Asn Asn Asp Lys Leu Arg Val Asn Gln Thr Thr Arg Lys Arg
 65 70 75 80
 gtc aga aaa atg gga cga aaa gta acc ttt gat gaa aag agg cag att 288
 Val Arg Lys Met Gly Arg Lys Val Thr Phe Asp Glu Lys Arg Gln Ile
 85 90 95
 gtc cga tgg aca att gaa cat aac aat aac tat aaa gcg gct gca gag 336
 Val Arg Trp Thr Ile Glu His Asn Asn Asn Tyr Lys Ala Ala Ala Glu
 100 105 110
 aag tat gat att agt tac caa cga gtt tat tct tgg gta cgg aag tac 384
 Lys Tyr Asp Ile Ser Tyr Gln Arg Val Tyr Ser Trp Val Arg Lys Tyr
 115 120 125
 cga gta aat agc gac tgg gaa gta cta aaa gat aac cgt ggg cgt aat 432
 Arg Val Asn Ser Asp Trp Glu Val Leu Lys Asp Asn Arg Gly Arg Asn
 130 135 140
 aaa gga aaa gag ccc act aat gaa cta gaa aaa cta agg aaa cga gtt 480
 Lys Gly Lys Glu Pro Thr Asn Glu Leu Glu Lys Leu Arg Lys Arg Val
 145 150 155 160
 cgt gag cta gaa gat cgt gac cgt gaa cgg gag ctg caa atc gct ttc 528
 Arg Glu Leu Glu Asp Arg Asp Arg Glu Arg Glu Leu Gln Ile Ala Phe
 165 170 175
 gca aaa aaa tta gtc gaa ata cgc aat cgg gag gtg aaa cga ccg gac 576
 Ala Lys Lys Leu Val Glu Ile Arg Asn Arg Glu Val Lys Arg Pro Asp
 180 185 190

gat atc aag cga ttc aag aaa tga
 Asp Ile Lys Arg Phe Lys Lys
 195

600

<210> 30
 <211> 199
 <212> PRT
 <213> Lactobacillus reuteri

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 Ala Val Lys Ala Tyr Leu Ser Gly Lys Tyr Thr Asn Gln Ala Ile Leu
 35 40 45
 Gln Gln Tyr Gln Ile Arg Asn Ile Ser Gln Leu His Gln Trp Val Ile
 50 55 60
 Ser Tyr Asn Asn Asp Lys Leu Arg Val Asn Gln Thr Thr Arg Lys Arg
 65 70 75 80
 Val Arg Lys Met Gly Arg Lys Val Thr Phe Asp Glu Lys Arg Gln Ile
 85 90 95
 Val Arg Trp Thr Ile Glu His Asn Asn Asn Tyr Lys Ala Ala Ala Glu
 100 105 110
 Lys Tyr Asp Ile Ser Tyr Gln Arg Val Tyr Ser Trp Val Arg Lys Tyr
 115 120 125
 Arg Val Asn Ser Asp Trp Glu Val Leu Lys Asp Asn Arg Gly Arg Asn
 130 135 140
 Lys Gly Lys Glu Pro Thr Asn Glu Leu Glu Lys Leu Arg Lys Arg Val
 145 150 155 160
 Arg Glu Leu Glu Asp Arg Asp Arg Glu Arg Glu Leu Gln Ile Ala Phe
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 180 185 190
 Asp Ile Lys Arg Phe Lys Lys
 195

<210> 31
 <211> 849
 <212> DNA
 <213> Lactobacillus reuteri

<220>
 <221> CDS
 <222> (1)..(849)

<400> 31

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1 5 10 15	
att act aga cag gct tac tac aaa tgg ttg aaa cat gaa ccg act aaa	96
Ile Thr Arg Gln Ala Tyr Tyr Lys Trp Leu Lys His Glu Pro Thr Lys	
20 25 30	
tat gag att gaa gaa tcg gag att ctc caa ttg att aaa cag tta gaa	144
Tyr Glu Ile Glu Glu Ser Glu Ile Leu Gln Leu Ile Lys Gln Leu Glu	
35 40 45	
aat gaa cat aag caa agc gtt ggt tat gac aaa atg act agg tta atc	192
Asn Glu His Lys Gln Ser Val Gly Tyr Asp Lys Met Thr Arg Leu Ile	
50 55 60	
aag tta agt cag cag atc tct tat acc gtt aat aag aaa cga gtc att	240
Lys Leu Ser Gln Gln Ile Ser Tyr Thr Val Asn Lys Lys Arg Val Ile	
65 70 75 80	
cgt att atg aaa ggc cat agt atc aag gcc gac tat cgt cag cca acc	288
Arg Ile Met Lys Gly His Ser Ile Lys Ala Asp Tyr Arg Gln Pro Thr	
85 90 95	
gac aaa cgt att caa gcc cag caa act tat gaa gct gaa aat att ctt	336
Asp Lys Arg Ile Gln Ala Gln Gln Thr Tyr Glu Ala Glu Asn Ile Leu	
100 105 110	
aac cga caa ttt gac caa act gca gct aac caa gtt tgg gtt acg gat	384
Asn Arg Gln Phe Asp Gln Thr Ala Ala Asn Gln Val Trp Val Thr Asp	
115 120 125	
acg acg gaa ctg aat tac gga atc tgg ctt aat aaa gtt cgt cta cat	432
Thr Thr Glu Leu Asn Tyr Gly Ile Trp Leu Asn Lys Val Arg Leu His	
130 135 140	
ata gta tta gat tta tat ggt caa tac cca gta agc tgg tta att aca	480
Ile Val Leu Asp Leu Tyr Gly Gln Tyr Pro Val Ser Trp Leu Ile Thr	
145 150 155 160	
cct aca gaa acc gct gaa gga gta gtt caa gtg ttc gag caa gca cgg	528
Pro Thr Glu Thr Ala Glu Gly Val Val Gln Val Phe Glu Gln Ala Arg	
165 170 175	
atg aaa gaa gga gca cta gct ccg tta att cat act gat cgt ggt gcg	576
Met Lys Glu Gly Ala Leu Ala Pro Leu Ile His Thr Asp Arg Gly Ala	
180 185 190	
gcg tat act tcc aaa gca ttt aat cag tat tta gta gtt aat ggt gcc	624
Ala Tyr Thr Ser Lys Ala Phe Asn Gln Tyr Leu Val Val Asn Gly Ala	
195 200 205	
caa cac agt tat tca gca cca ggg aca ccg gct gac aat gcc gta ata	672
Gln His Ser Tyr Ser Ala Pro Gly Thr Pro Ala Asp Asn Ala Val Ile	
210 215 220	
gaa cat tgg tgg gca gat ttt aag gct att tgg atc gca cat cta cct	720
Glu His Trp Trp Ala Asp Phe Lys Ala Ile Trp Ile Ala His Leu Pro	
225 230 235 240	

aaa gca caa aca tta tta gaa cta gaa gaa caa gtt aga gaa gga att 768
 Lys Ala Gln Thr Leu Leu Glu Leu Glu Glu Gln Val Arg Glu Gly Ile
 245 250 255

acc tat ttc act gaa aaa ttt atc tca gcg aag aga aat gac ctt acc 816
 Thr Tyr Phe Thr Glu Lys Phe Ile Ser Ala Lys Arg Asn Asp Leu Thr
 260 265 270

gca gcg gaa tac cgc ttt ggc aag gcc aac taa 849
 Ala Ala Glu Tyr Arg Phe Gly Lys Ala Asn
 275 280

<210> 32
 <211> 282
 <212> PRT
 <213> Lactobacillus reuteri

<400> 32
 Met Asn Asn Glu Gly Tyr Ser Ile Ser Glu Leu Ala Lys Val Ala Gly
 1 5 10 15
 Ile Thr Arg Gln Ala Tyr Tyr Lys Trp Leu Lys His Glu Pro Thr Lys
 20 25 30
 Tyr Glu Ile Glu Glu Ser Glu Ile Leu Gln Leu Ile Lys Gln Leu Glu
 35 40 45
 Asn Glu His Lys Gln Ser Val Gly Tyr Asp Lys Met Thr Arg Leu Ile
 50 55 60
 Lys Leu Ser Gln Gln Ile Ser Tyr Thr Val Asn Lys Lys Arg Val Ile
 65 70 75 80
 Arg Ile Met Lys Gly His Ser Ile Lys Ala Asp Tyr Arg Gln Pro Thr
 85 90 95
 Asp Lys Arg Ile Gln Ala Gln Gln Thr Tyr Glu Ala Glu Asn Ile Leu
 100 105 110
 Asn Arg Gln Phe Asp Gln Thr Ala Ala Asn Gln Val Trp Val Thr Asp
 115 120 125
 Thr Thr Glu Leu Asn Tyr Gly Ile Trp Leu Asn Lys Val Arg Leu His
 130 135 140
 Ile Val Leu Asp Leu Tyr Gly Gln Tyr Pro Val Ser Trp Leu Ile Thr
 145 150 155 160
 Pro Thr Glu Thr Ala Glu Gly Val Val Gln Val Phe Glu Gln Ala Arg
 165 170 175
 Met Lys Glu Gly Ala Leu Ala Pro Leu Ile His Thr Asp Arg Gly Ala
 180 185 190
 Ala Tyr Thr Ser Lys Ala Phe Asn Gln Tyr Leu Val Val Asn Gly Ala
 195 200 205
 Gln His Ser Tyr Ser Ala Pro Gly Thr Pro Ala Asp Asn Ala Val Ile
 210 215 220
 Glu His Trp Trp Ala Asp Phe Lys Ala Ile Trp Ile Ala His Leu Pro
 225 230 235 240
 Lys Ala Gln Thr Leu Leu Glu Leu Glu Gln Val Arg Glu Gly Ile
 245 250 255
 Thr Tyr Phe Thr Glu Lys Phe Ile Ser Ala Lys Arg Asn Asp Leu Thr
 260 265 270
 Ala Ala Glu Tyr Arg Phe Gly Lys Ala Asn
 275 280

<210> 33
 <211> 744
 <212> DNA

<213> Lactobacillus reuteri

<220>

<221> CDS

<222> (1)..(744)

<220>

<221> unsure

<222> (1)..(744)

<223> n = a, c, g, or t

<400> 33

atg ctt cgt tan acc ata tta gta aaa ttg ctt att gga aga aaa cca	48
Met Leu Arg Xaa Thr Ile Leu Val Lys Leu Leu Ile Gly Arg Lys Pro	
1 5 10 15	
gtc aca acg atc aaa aaa aca tta ccg cca act cag gaa cag gct aat	96
Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn	
20 25 30	
tca gtc tta act ccg gct gtt cgc caa caa ctt ggc att tca att acc	144
Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr	
35 40 45	
tgg aac aaa gcc ggt gcg ttt att atc aat aat aac caa aca aat ctt	192
Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Gln Thr Asn Leu	
50 55 60	
aac gct aag att gca agt gca ccc tat gct gta aat cat ctt gac cgt	240
Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg	
65 70 75 80	
caa gga agg gcg tgg caa ggt gat gcc tgg tta aac agg aca act cgg	288
Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg	
85 90 95	
tca ata tan aag ccg aaa ttt gcc aca ggg aat ggt gct acg gat tgg	336
Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp	
100 105 110	
cga cca gct ggc ttc ctt cag gcg cat aat ctt aaa ggc ggg tac aat	384
Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn	
115 120 125	
cat gca tac gat cgc gga cac ctt ctt gcc tat gca cta gtt ggt ggt	432
His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly	
130 135 140	
att cat gga ttt gat gca tcc gaa tca aat cca tct aat att gcc acg	480
Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr	
145 150 155 160	
caa act gcc tgg gca aat gaa gca cga agt aag aac tca aca ggg caa	528
Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln	
165 170 175	
aat tac tac gaa ggt ctg gtg aga aaa gca tta gat cag aat aag caa	576
Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln	
180 185 190	
gtt cgc tac cga gtt acc aat att tat gac ggt aat aat atc gtt ccg	624

Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro
 195 200 205

gca ggt gct cat atc gaa gct aaa tct agt gat ggt tct cta gaa tac 672
 Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr
 210 215 220

aat gtc ttt gtt ccg aat gtc caa aga aac att acc att aat tat tca 720
 Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser
 225 230 235 240

acc ggt gca gta aaa caa aac taa 744
 Thr Gly Ala Val Lys Gln Asn
 245

<210> 34
 <211> 247
 <212> PRT
 <213> Lactobacillus reuteri

<220>
 <221> UNSURE
 <222> (1)..(247)
 <223> Xaa = Tyr or stop

<400> 34
 Met Leu Arg Xaa Thr Ile Leu Val Lys Leu Leu Ile Gly Arg Lys Pro
 1 5 10 15
 Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn
 20 25 30
 Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr
 35 40 45
 Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu
 50 55 60
 Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg
 65 70 75 80
 Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg
 85 90 95
 Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp
 100 105 110
 Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn
 115 120 125
 His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly
 130 135 140
 Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr
 145 150 155 160
 Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln
 165 170 175
 Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln
 180 185 190
 Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro
 195 200 205
 Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr
 210 215 220
 Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser
 225 230 235 240
 Thr Gly Ala Val Lys Gln Asn
 245

<210> 35
 <211> 1540
 <212> DNA
 <213> Lactobacillus reuteri

<220>
 <221> CDS
 <222> (1)..(1539)

<400> 35
 atg gtc atg aca gaa act gct ggt ata aga aaa att cat att gtt ttt 48
 Met Val Met Thr Glu Thr Ala Gly Ile Arg Lys Ile His Ile Val Phe
 1 5 10 15
 gat ggt caa gaa aca cca cca tta aag atc cat caa tta ttt gat tca 96
 Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser
 20 25 30
 caa aaa tac gat cag tta atc gca gta act ggg aaa att act gct gac 144
 Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp
 35 40 45
 ttc att aat aaa tac ctt agt aat ttt atc agt att aat gta gcg tta 192
 Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu
 50 55 60
 agc tcc caa tca act agt gaa tta agt gct gat gag atg gtg aca aag 240
 Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys
 65 70 75 80
 gtt gca ctt acc aat gct ctc ctt agt tca gca aat aaa gaa gct gct 288
 Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala
 85 90 95
 aaa ctc ttc tca gcg tta acc agt gac aac caa acg aac gtc tta aat 336
 Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn
 100 105 110
 aat gtt ttt cgc gta tca atc gcg cct act cag gtt atc cat tct aag 384
 Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys
 115 120 125
 ttt tac ttg tta agt agt tca act act cat gat tcc cgt gtg att ctt 432
 Phe Tyr Leu Leu Ser Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu
 130 135 140
 ggg agt gta gat tta gac gaa gct tca ttt gat gct cac cga aat caa 480
 Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln
 145 150 155 160
 ttt gaa gaa gta ttg gta ttt gac aat gat gtc cgc tta tac caa aac 528
 Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn
 165 170 175
 ctt act gac cac ttt aaa aag gat ttt aag cca gta ttg aag ccc ttc 576
 Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe
 180 185 190
 ttt act atg aac cta gta aag gca gct caa aag caa gtt gag gaa gga 624
 Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly

195	200	205	
aag aaa gat cag gat agc ggt aag gga ccg gtt atc ctt gat aat gaa Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro Val Ile Leu Asp Asn Glu 210 215 220			672
aca aca gat aag atc gct gaa aca gac atg gtg gat ctg ttg aag cat Thr Thr Asp Lys Ile Ala Glu Thr Asp Met Val Asp Leu Leu Lys His 225 230 235 240			720
gac ctt cag cat gat att gac cat aat ctt gtt cct gaa atg atc aca Asp Leu Gln His Asp Ile Asp His Asn Leu Val Pro Glu Met Ile Thr 245 250 255			768
aag tca atg cgt gat att acc ata aat cgt tct caa gca aag gag aaa Lys Ser Met Arg Asp Ile Thr Ile Asn Arg Ser Gln Ala Lys Glu Lys 260 265 270			816
att gct aag cag gtt aag caa cat gat acg att tat act ttg caa aaa Ile Ala Lys Gln Val Lys Gln His Asp Thr Ile Tyr Thr Leu Gln Lys 275 280 285			864
gaa gcg gtc tct cct cgg gca gct aag cca aaa cta aag act cga gaa Glu Ala Val Ser Pro Arg Ala Ala Lys Pro Lys Leu Lys Thr Arg Glu 290 295 300			912
aaa att acc aag cag gtt cag gat gct ttg atc agt gga atg tca cca Lys Ile Thr Lys Gln Val Gln Asp Ala Leu Ile Ser Gly Met Ser Pro 305 310 315 320			960
cag caa cgg gat gct gag aaa aag tac acg act ttt ctg tac gat cgg Gln Gln Arg Asp Ala Glu Lys Lys Tyr Thr Thr Phe Leu Tyr Asp Arg 325 330 335			1008
cca atg gaa cga aac att gcg aat aac aat agt ggc cta tac gtt cct Pro Met Glu Arg Asn Ile Ala Asn Asn Asn Ser Gly Leu Tyr Val Pro 340 345 350			1056
aat gat acg gga act cac cca atc cca ttt ggt aaa att gca act att Asn Asp Thr Gly Thr His Pro Ile Pro Phe Gly Lys Ile Ala Thr Ile 355 360 365			1104
tct gaa att cgt gac ggt tta aag agc att gat gct gtt atg aag ggc Ser Glu Ile Arg Asp Gly Leu Lys Ser Ile Asp Ala Val Met Lys Gly 370 375 380			1152
tat cag cag ttt gtc gtt gat tat gat gct gac tac ggg aag cgg ttc Tyr Gln Gln Phe Val Val Asp Tyr Asp Ala Asp Tyr Gly Lys Arg Phe 385 390 395 400			1200
ttt gaa gca att ttg tat agt ttt act gca ccg ttt tta tgg gaa att Phe Glu Ala Ile Leu Tyr Ser Phe Thr Ala Pro Phe Leu Trp Glu Ile 405 410 415			1248
cgt tct aaa gct agc ctg aac cct gaa gat ggg aat gat gtt cct aat Arg Ser Lys Ala Ser Leu Asn Pro Glu Asp Gly Asn Asp Val Pro Asn 420 425 430			1296
ttc cta atc cta ggg gca acg gct ggt tcc gga aag tct acc ctt ctt Phe Leu Ile Leu Gly Ala Thr Ala Gly Ser Gly Lys Ser Thr Leu Leu 435 440 445			1344

cgg att att aat cag ctc acg tgg aac act gat cgc tcg ttg att gac 1392
 Arg Ile Ile Asn Gln Leu Thr Trp Asn Thr Asp Arg Ser Leu Ile Asp
 450 455 460

ttt gga acg atc tac ccg tcg caa act cct caa aag aag gca aag act 1440
 Phe Gly Thr Ile Tyr Pro Ser Gln Thr Pro Gln Lys Lys Ala Lys Thr
 465 470 475 480

gtt gag gcg atg gaa cat tat atg aaa ctt ggt agt tca tac ccg gtt 1488
 Val Glu Ala Met Glu His Tyr Met Lys Leu Gly Ser Ser Tyr Pro Val
 485 490 495

ttg tta gat gaa att gaa ccg tac ttc ttc cag caa gat caa tat agt 1536
 Leu Leu Asp Glu Ile Glu Pro Tyr Phe Phe Gln Gln Asp Gln Tyr Ser
 500 505 510

cga c 1540
 Arg

<210> 36

<211> 513

<212> PRT

<213> Lactobacillus reuteri

<400> 36

Met Val Met Thr Glu Thr Ala Gly Ile Arg Lys Ile His Ile Val Phe
 1 5 10 15

Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser
 20 25 30

Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp
 35 40 45

Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu
 50 55 60

Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys
 65 70 75 80

Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala
 85 90 95

Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn
 100 105 110

Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys
 115 120 125

Phe Tyr Leu Leu Ser Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu
 130 135 140

Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln
 145 150 155 160

Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn
 165 170 175

Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe

180										185					190				
Phe	Thr	Met	Asn	Leu	Val	Lys	Ala	Ala	Gln	Lys	Gln	Val	Glu	Glu	Gly				
		195					200					205							
Lys	Lys	Asp	Gln	Asp	Ser	Gly	Lys	Gly	Pro	Val	Ile	Leu	Asp	Asn	Glu				
	210					215					220								
Thr	Thr	Asp	Lys	Ile	Ala	Glu	Thr	Asp	Met	Val	Asp	Leu	Leu	Lys	His				
225					230					235					240				
Asp	Leu	Gln	His	Asp	Ile	Asp	His	Asn	Leu	Val	Pro	Glu	Met	Ile	Thr				
			245					250						255					
Lys	Ser	Met	Arg	Asp	Ile	Thr	Ile	Asn	Arg	Ser	Gln	Ala	Lys	Glu	Lys				
			260					265					270						
Ile	Ala	Lys	Gln	Val	Lys	Gln	His	Asp	Thr	Ile	Tyr	Thr	Leu	Gln	Lys				
		275					280					285							
Glu	Ala	Val	Ser	Pro	Arg	Ala	Ala	Lys	Pro	Lys	Leu	Lys	Thr	Arg	Glu				
	290					295					300								
Lys	Ile	Thr	Lys	Gln	Val	Gln	Asp	Ala	Leu	Ile	Ser	Gly	Met	Ser	Pro				
305				310						315					320				
Gln	Gln	Arg	Asp	Ala	Glu	Lys	Lys	Tyr	Thr	Thr	Phe	Leu	Tyr	Asp	Arg				
			325					330						335					
Pro	Met	Glu	Arg	Asn	Ile	Ala	Asn	Asn	Asn	Ser	Gly	Leu	Tyr	Val	Pro				
			340				345						350						
Asn	Asp	Thr	Gly	Thr	His	Pro	Ile	Pro	Phe	Gly	Lys	Ile	Ala	Thr	Ile				
		355				360						365							
Ser	Glu	Ile	Arg	Asp	Gly	Leu	Lys	Ser	Ile	Asp	Ala	Val	Met	Lys	Gly				
	370					375					380								
Tyr	Gln	Gln	Phe	Val	Val	Asp	Tyr	Asp	Ala	Asp	Tyr	Gly	Lys	Arg	Phe				
385				390					395					400					
Phe	Glu	Ala	Ile	Leu	Tyr	Ser	Phe	Thr	Ala	Pro	Phe	Leu	Trp	Glu	Ile				
			405					410					415						
Arg	Ser	Lys	Ala	Ser	Leu	Asn	Pro	Glu	Asp	Gly	Asn	Asp	Val	Pro	Asn				
			420					425					430						
Phe	Leu	Ile	Leu	Gly	Ala	Thr	Ala	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu				
		435					440					445							
Arg	Ile	Ile	Asn	Gln	Leu	Thr	Trp	Asn	Thr	Asp	Arg	Ser	Leu	Ile	Asp				
	450					455					460								
Phe	Gly	Thr	Ile	Tyr	Pro	Ser	Gln	Thr	Pro	Gln	Lys	Lys	Ala	Lys	Thr				
465				470					475					480					
Val	Glu	Ala	Met	Glu	His	Tyr	Met	Lys	Leu	Gly	Ser	Ser	Tyr	Pro	Val				
			485					490						495					
Leu	Leu	Asp	Glu	Ile	Glu	Pro	Tyr	Phe	Phe	Gln	Gln	Asp	Gln	Tyr	Ser				
		500						505					510						

Arg

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<210> 37
<211> 26
<212> DNA
<213> Lactobacillus reuteri

<220>
<221> terminator
<222> (1)..(26)

<400> 37
aaagaagctg aaatttcggc ttcttt

26

<210> 38
<211> 28
<212> DNA
<213> Lactobacillus reuteri

<400> 38
gcagtcgacg gagttaagac tgaattag

28

<210> 39
<211> 26
<212> DNA
<213> Lactobacillus reuteri

<400> 39
ctagtcgacg cagtttctgt catgac

26

<210> 40
<211> 32
<212> DNA
<213> Lactobacillus reuteri

<400> 40
catatgtatt attcaaacgg gaattatgaa gc

32

<210> 41
<211> 30
<212> DNA
<213> Lactobacillus reuteri

<400> 41
tgatcatcta taccagcagt ttctgtcatg

30

<210> 42
<211> 35
<212> PRT
<213> Propionibacterium acnes

<220>

<221> UNSURE

<222> (30)

<223> Xaa = any amino acid

<400> 42

Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro Ala
1 5 10 15

Gly Leu Ala Ala Gly Met Tyr Leu Trp Gln Ala Gly Phe Xaa Asp Tyr
20 25 30

Thr Ile Leu
35

<210> 43

<211> 21

<212> PRT

<213> Clostridium sporogenes

<220>

<221> UNSURE

<222> (18)

<223> Xaa = any amino acid

<400> 43

Met Phe Asn Leu Lys Asn Arg Asn Phe Leu Thr Leu Met Asp Phe Thr
1 5 10 15

Pro Xaa Glu Ile Gln
20

<210> 44

<211> 14

<212> PRT

<213> Propionibacterium acnes

<400> 44

Lys Tyr Leu Asp Phe Val Thr Met Met Ser Phe Ala Lys Gly
1 5 10

<210> 45

<211> 9

<212> PRT

<213> Propionibacterium acnes

<400> 45

Lys Asp Leu Val Thr Arg Phe Phe Val
1 5

<210> 46

<211> 15

<212> PRT

<213> Propionibacterium acnes

<220>

<221> UNSURE

<222> (2)

<223> Xaa = Ile or Ser

<220>

<221> UNSURE

<222> (4)

<223> Xaa = His or Phe

<220>

<221> UNSURE

<222> (6)

<223> Xaa = Glu or Gln

<220>

<221> UNSURE

<222> (10)

<223> Xaa = Asp or Thr

<220>

<221> UNSURE

<222> (12)

<223> Xaa = Gly or Ser

<400> 46

Lys	Xaa	Ile	Xaa	Gln	Xaa	Tyr	Met	Val	Xaa	Ala	Xaa	Leu	Val	Lys
1				5					10					15

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> unsure

<222> (1)..(20)

<223> n = a, c, g, or t

<400> 47

atcgcgatna tnggngcngg

20

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> unsure

<222> (1)..(20)

<223> n = a, c, g, or t

<400> 48

ccngcytgcc anarrtacat

20

<210> 49
<211> 62
<212> DNA
<213> Propionibacterium acnes

<400> 49
atcgagatva trggggctgg cccggccggg ctggctgccg gaatgtacct ctggcargcs 60
gg 62

<210> 50
<211> 21
<212> PRT
<213> Propionibacterium acnes

<220>
<221> UNSURE
<222> (2)
<223> xaa = ala or glu

<220>
<221> UNSURE
<222> (3)..(4)
<223> xaa = ile or met

<400> 50
Ile Xaa Xaa Xaa Gly Ala Gly Pro Ala Gly Leu Ala Ala Gly Met Tyr
1 5 10 15

Leu Trp Gln Ala Gly
20

<210> 51
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> unsure
<222> (1)..(17)
<223> n = a, c, g, or t

<400> 51
gggccagccc cyatnat

17

<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 52
gctggctgcc ggaatgta

18

<210> 53
 <211> 569
 <212> DNA
 <213> Propionibacterium acnes

<400> 53
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 ggccaaggag ctggcagcac atctcgatga gatggcacgt ggtcggcgaa ctgcccgtg 180
 agatgtttcg cgacctatac cattaccgac ccatttcac gccgaactta ttcaccacta 240
 catcgacaag gaagaacgat gtccatctcg aaggattcac gtatcgccat catcggggct 300
 ggcccggccg ggctggctgc cggaatgtac ctggaacagg ccggatttca cgactacacg 360
 atcctggaac gcaccgacca cgtcggaggc aagtgccact caccgaacta ccacggccgt 420
 cgttatgaga tgggggccat catgggcgtc ccagttacg acaccatcca ggagatcatg 480
 gatcgactg gcgacaaggc cgacgggccc aaactgcgtc gcgagttcct gcacgaggac 540
 ggcgagatct acgtcccgga aaaggatcc 569

<210> 54
 <211> 104
 <212> PRT
 <213> Propionibacterium acnes

<400> 54
 Met Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro
 1 5 10 15
 Ala Gly Leu Ala Ala Gly Met Tyr Leu Glu Gln Ala Gly Phe His Asp
 20 25 30
 Tyr Thr Ile Leu Glu Arg Thr Asp His Val Gly Gly Lys Cys His Ser
 35 40 45
 Pro Asn Tyr His Gly Arg Arg Tyr Glu Met Gly Ala Ile Met Gly Val
 50 55 60
 Pro Ser Tyr Asp Thr Ile Gln Glu Ile Met Asp Arg Thr Gly Asp Lys
 65 70 75 80
 Val Asp Gly Pro Lys Leu Arg Arg Glu Phe Leu His Glu Asp Gly Glu
 85 90 95
 Ile Tyr Val Pro Glu Lys Asp Pro
 100

<210> 55
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 55
 cgatgtcggc gtggtac

<210> 56
 <211> 18

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 56

tcacgtatcg ccatcatc

18

<210> 57

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 57

aatccggcct gttcgag

17

<210> 58

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 58

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17

<210> 59

<211> 5275

<212> DNA

<213> Propionibacterium acnes

<400> 59

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atctggggcg tctcgtcagg gccggatcca taccggaccg ttctcgtcagg gtggtcggac 660
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ctcgggcatg	gtgcgcgcag	aaaaggagct	cgccaccgtt	gcgcagcgtg	atgcgcacat	4920

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aggcttgtgc gccgcaacga tcacaacggt ccgcagtggt aagggcttgg tgttcgatca 4980
tcgtggtgct catgacaacc tcctccatct gaatcatcgg atcacctact agacaacctta 5040
cgctatcgtc ggaatgttct catacgtatc gaaagatgga tggctggggg cgaacacggt 5100
gccgggattc cgtgtcgtcg gctgtcgata agctgccacc gtgaccatgg acaacatctc 5160
gacctcatca gccaacagct cggaaacgcc acgtggtaag ggcgataccg tgcgcacggc 5220
gtcgactagc cgggagtacg gcgccaagaa tttattgggt ttggaggggc tcgag 5275

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<210> 60
 <211> 1275
 <212> DNA
 <213> *Propionibacterium acnes*

<220>
 <221> CDS
 <222> (1)..(1272)

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Met Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro
1 5 10 15

gcc ggg ctg gct gcc gga atg tac ctc gaa cag gcc gga ttt cac gac 96
Ala Gly Leu Ala Ala Gly Met Tyr Leu Glu Gln Ala Gly Phe His Asp
20 25 30

tac acg atc ctg gaa cgc acc gac cac gtc gga ggc aag tgc cac tca 144
Tyr Thr Ile Leu Glu Arg Thr Asp His Val Gly Gly Lys Cys His Ser
35 40 45

ccg aac tac cac ggc cgt cgt tat gag atg ggg gcc atc atg ggc gtc 192
Pro Asn Tyr His Gly Arg Arg Tyr Glu Met Gly Ala Ile Met Gly Val
50 55 60

ccc agt tac gac acc atc cag gag atc atg gat cgc act ggc gac aag 240
Pro Ser Tyr Asp Thr Ile Gln Glu Ile Met Asp Arg Thr Gly Asp Lys
65 70 75 80

gtc gac ggg ccg aaa ctg cgt cgc gag ttc ctg cac gag gac ggc gag 288
Val Asp Gly Pro Lys Leu Arg Arg Glu Phe Leu His Glu Asp Gly Glu
85 90 95

atc tac gtc ccg gaa aag gat cca gtg cgt ggt ccg cag gtc atg gca 336
Ile Tyr Val Pro Glu Lys Asp Pro Val Arg Gly Pro Gln Val Met Ala
100 105 110

gca gtg cag aag ctg ggc cag ttg ctc gcg acg aag tac cag gga tat 384
Ala Val Gln Lys Leu Gly Gln Leu Leu Ala Thr Lys Tyr Gln Gly Tyr
115 120 125

gac gcc aac ggc cac tac aac aag gtt cac gag gac ctc atg ctg ccc 432
Asp Ala Asn Gly His Tyr Asn Lys Val His Glu Asp Leu Met Leu Pro
130 135 140

ttc gac gag ttc ctc gcc ctc aac ggg tgc gag gcc gcc cga gac ctg 480
Phe Asp Glu Phe Leu Ala Leu Asn Gly Cys Glu Ala Ala Arg Asp Leu
145 150 155 160

tgg atc aac ccc ttc acg gcc ttc ggc tac ggg cac ttc gac aac gtc 528
Trp Ile Asn Pro Phe Thr Ala Phe Gly Tyr Gly His Phe Asp Asn Val
165 170 175

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ccg gcc gcc tac gtg ctg aag tac ctc gac ttc gtc acc atg atg tcc	576
Pro Ala Ala Tyr Val Leu Lys Tyr Leu Asp Phe Val Thr Met Met Ser	
180 185 190	
ttt gcc aag gga gat ctg tgg acg tgg gcc gac ggc acc cag gcg atg	624
Phe Ala Lys Gly Asp Leu Trp Thr Trp Ala Asp Gly Thr Gln Ala Met	
195 200 205	
ttc gag cac ctc aac gcc acc ctg gag cac ccg gcc gaa cgc aac gtt	672
Phe Glu His Leu Asn Ala Thr Leu Glu His Pro Ala Glu Arg Asn Val	
210 215 220	
gac atc act cgc atc acc cgc gag gac ggc aag gtc cac att cac acc	720
Asp Ile Thr Arg Ile Thr Arg Glu Asp Gly Lys Val His Ile His Thr	
225 230 235 240	
acg gac tgg gat cgc gag tcc gac gtc ctc gtc ctc acc gtc ccg ctg	768
Thr Asp Trp Asp Arg Glu Ser Asp Val Leu Val Leu Thr Val Pro Leu	
245 250 255	
gaa aag ttc ctc gac tac tcc gac gcg gac gat gac gag cgg gag tac	816
Glu Lys Phe Leu Asp Tyr Ser Asp Ala Asp Asp Asp Glu Arg Glu Tyr	
260 265 270	
ttc tcg aag atc atc cac cag cag tac atg gtg gat gcc tgc ctg gtg	864
Phe Ser Lys Ile Ile His Gln Gln Tyr Met Val Asp Ala Cys Leu Val	
275 280 285	
aag gag tac ccg acc atc tcc ggg tac gtc ccc gac aac atg agg ccc	912
Lys Glu Tyr Pro Thr Ile Ser Gly Tyr Val Pro Asp Asn Met Arg Pro	
290 295 300	
gaa cgt ctc ggg cac gtc atg gtt tac tac cac cgc tgg gct gat gat	960
Glu Arg Leu Gly His Val Met Val Tyr Tyr His Arg Trp Ala Asp Asp	
305 310 315 320	
ccg cac cag atc atc acg acc tac ctg cta cgt aac cat ccg gac tac	1008
Pro His Gln Ile Ile Thr Thr Tyr Leu Leu Arg Asn His Pro Asp Tyr	
325 330 335	
gcg gac aag act cag gag gag tgc cgc cag atg gtc ctc gac gac atg	1056
Ala Asp Lys Thr Gln Glu Glu Cys Arg Gln Met Val Leu Asp Asp Met	
340 345 350	
gag acc ttc ggt cat ccg gtc gag aag atc atc gag gag cag acc tgg	1104
Glu Thr Phe Gly His Pro Val Glu Lys Ile Ile Glu Glu Gln Thr Trp	
355 360 365	
tac tac ttc ccg cac gtt agc tcg gag gac tac aag gcc ggg tgg tac	1152
Tyr Tyr Phe Pro His Val Ser Ser Glu Asp Tyr Lys Ala Gly Trp Tyr	
370 375 380	
gag aag gtc gag gga atg cag ggt cgt cgc aac acc ttc tac gcc gga	1200
Glu Lys Val Glu Gly Met Gln Gly Arg Arg Asn Thr Phe Tyr Ala Gly	
385 390 395 400	
gaa att atg agt ttc ggt aat ttc gac gag gtg tgc cac tac tcg aag	1248
Glu Ile Met Ser Phe Gly Asn Phe Asp Glu Val Cys His Tyr Ser Lys	
405 410 415	

gac ctg gtg acg cgg ttc ttc gtg tga
 Asp Leu Val Thr Arg Phe Phe Val
 420

1275

<210> 61
 <211> 424
 <212> PRT
 <213> Propionibacterium acnes

<400> 61

Met Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro
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 Ala Gly Leu Ala Ala Gly Met Tyr Leu Glu Gln Ala Gly Phe His Asp
 20 25 30
 Tyr Thr Ile Leu Glu Arg Thr Asp His Val Gly Gly Lys Cys His Ser
 35 40 45
 Pro Asn Tyr His Gly Arg Arg Tyr Glu Met Gly Ala Ile Met Gly Val
 50 55 60
 Pro Ser Tyr Asp Thr Ile Gln Glu Ile Met Asp Arg Thr Gly Asp Lys
 65 70 75 80
 Val Asp Gly Pro Lys Leu Arg Arg Glu Phe Leu His Glu Asp Gly Glu
 85 90 95
 Ile Tyr Val Pro Glu Lys Asp Pro Val Arg Gly Pro Gln Val Met Ala
 100 105 110
 Ala Val Gln Lys Leu Gly Gln Leu Leu Ala Thr Lys Tyr Gln Gly Tyr
 115 120 125
 Asp Ala Asn Gly His Tyr Asn Lys Val His Glu Asp Leu Met Leu Pro
 130 135 140
 Phe Asp Glu Phe Leu Ala Leu Asn Gly Cys Glu Ala Ala Arg Asp Leu
 145 150 155 160
 Trp Ile Asn Pro Phe Thr Ala Phe Gly Tyr Gly His Phe Asp Asn Val
 165 170 175
 Pro Ala Ala Tyr Val Leu Lys Tyr Leu Asp Phe Val Thr Met Met Ser
 180 185 190
 Phe Ala Lys Gly Asp Leu Trp Thr Trp Ala Asp Gly Thr Gln Ala Met
 195 200 205
 Phe Glu His Leu Asn Ala Thr Leu Glu His Pro Ala Glu Arg Asn Val
 210 215 220
 Asp Ile Thr Arg Ile Thr Arg Glu Asp Gly Lys Val His Ile His Thr
 225 230 235 240
 Thr Asp Trp Asp Arg Glu Ser Asp Val Leu Val Leu Thr Val Pro Leu
 245 250 255
 Glu Lys Phe Leu Asp Tyr Ser Asp Ala Asp Asp Asp Glu Arg Glu Tyr
 260 265 270

Phe Ser Lys Ile Ile His Gln Gln Tyr Met Val Asp Ala Cys Leu Val
 275 280 285
 Lys Glu Tyr Pro Thr Ile Ser Gly Tyr Val Pro Asp Asn Met Arg Pro
 290 295 300
 Glu Arg Leu Gly His Val Met Val Tyr Tyr His Arg Trp Ala Asp Asp
 305 310 315 320
 Pro His Gln Ile Ile Thr Thr Tyr Leu Leu Arg Asn His Pro Asp Tyr
 325 330 335
 Ala Asp Lys Thr Gln Glu Glu Cys Arg Gln Met Val Leu Asp Asp Met
 340 345 350
 Glu Thr Phe Gly His Pro Val Glu Lys Ile Ile Glu Glu Gln Thr Trp
 355 360 365
 Tyr Tyr Phe Pro His Val Ser Ser Glu Asp Tyr Lys Ala Gly Trp Tyr
 370 375 380
 Glu Lys Val Glu Gly Met Gln Gly Arg Arg Asn Thr Phe Tyr Ala Gly
 385 390 395 400
 Glu Ile Met Ser Phe Gly Asn Phe Asp Glu Val Cys His Tyr Ser Lys
 405 410 415
 Asp Leu Val Thr Arg Phe Phe Val
 420

<210> 62
 <211> 7
 <212> DNA
 <213> Propionibacterium acnes

<220>
 <221> RBS
 <222> (1)..(7)
 <400> 62
 aaggaag

7

<210> 63
 <211> 1073
 <212> DNA
 <213> Propionibacterium acnes

<400> 63
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 gcgcgataac ggtcggggaa ttgcttgggg gtgccaccga tatacatttt ggccggcattg 180
 cccgcgctca gtgtggtgac cgactcgacg gtaccgacat ccaccgttgg atagagggcg 240
 aggactgact tcggggcccg tattgagccg caggaaactct tcaactttcc actggcggcg 300
 ccgtaggcga gattaatggc cattccacca ccagcgggaat caccatgat cgatacctgt 360
 gaagggtcgc caccgagttc ttccacgtgg gacaggctcc agggccaggc acatgcgacc 420
 tgttttgggg cggtattcca ggtgggggtg ccctgggtgg ccagggtgta cgaggggcga 480
 atgactaacc agccatgatc ggaaaacat ctcaacgtgg cgggcattgt ggcgtcgggtg 540

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ctccatcctt caccatgaat gtcgacaagt accggggcat tgtggttatg ggcacggtag 600
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gccaccactc gcagaccacc tcgtcccaaa agagcgagga cgaaggcgat gacggcgatg 840
accagagccg gtacagccaa cgatcccacc agaacggagg agatgaaggt gaggggcattg 900
tgtgagggga ggatcgcggc cactgaccac gccagtaccg gcagggtcag gatcagccccg 960
acgagaccgg aagtgatgcg tagccaggaa tgacgggagg ttttcgtgtc agccacgcgt 1020
ccaccgtact cacgggacat ggtcgatagg atcttcgcgc aggagggacc cat 1073

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<210> 64
 <211> 358
 <212> PRT
 <213> Propionibacterium acnes

<400> 64

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          20          25          30
Ile Thr Ser Gly Leu Val Gly Leu Ile Leu Thr Leu Pro Val Leu Ala
      35          40          45
Trp Ser Val Ala Ala Ile Leu Pro Ser His Asn Ala Leu Thr Phe Ile
      50          55          60
Ser Ser Val Leu Val Gly Ser Leu Ala Val Pro Ala Leu Val Ile Ala
      65          70          75          80
Val Ile Ala Phe Val Leu Ala Leu Leu Gly Arg Gly Gly Leu Arg Val
          85          90          95
Val Ala Val Val Phe Ser Val Met Ala Leu Ile Val Pro Val Ala Ala
          100         105         110
Thr Ala Thr Thr Ala Trp Ile Thr Asp Arg Pro Gly Gly Arg Ile Asn
      115         120         125
Val Val Ser Ala Ala Ala Val Ser Ser Met Ser Asp His Pro Asp Glu
      130         135         140
Thr Val Arg Tyr Gly Ser Gly Pro Asp Glu Thr Ala Gln Ile Tyr Arg
      145         150         155         160
Ala His Asn His Asn Ala Pro Val Leu Val Asp Ile His Gly Glu Gly
          165         170         175
Trp Ser Thr Asp Ala Thr Met Pro Ala Thr Leu Arg Trp Phe Ser Asp
      180         185         190
His Gly Trp Leu Val Ile Arg Pro Ser Tyr Thr Leu Ala Thr Gln Gly
      195         200         205
His Pro Thr Trp Asn Thr Ala Pro Lys Gln Val Ala Cys Ala Trp Ala
      210         215         220
Trp Ser Leu Ser His Val Lys Glu Leu Gly Gly Asp Pro Ser Gln Val
      225         230         235         240

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Ser Ile Met Gly Asp Ser Ala Gly Gly Gly Met Ala Ile Asn Leu Ala
 245 250 255
 Tyr Gly Ala Ala Ser Gly Lys Leu Lys Ser Ser Cys Gly Ser Ile Arg
 260 265 270
 Ala Pro Lys Ser Val Leu Ala Leu Tyr Pro Thr Val Asp Val Gly Thr
 275 280 285
 Val Glu Ser Val Thr Thr Leu Ser Ala Gly Asn Ala Ala Lys Met Tyr
 290 295 300
 Ile Gly Gly Thr Pro Lys Gln Phe Pro Asp Arg Tyr Arg Ala Val Asn
 305 310 315 320
 Ser Ser Thr Trp Ile Thr Pro Gln Ala Pro Pro Thr Met Val Ile Gln
 325 330 335
 Gly Asn His Asp Thr Phe Val Pro Pro Ser Ser Val Arg Lys Phe Val
 340 345 350
 Asn Arg Ala Arg Pro Ala
 355

<210> 65
 <211> 783
 <212> DNA
 <213> Propionibacterium acnes

<220>
 <221> CDS
 <222> (1)..(783)

<400> 65
 atg tcc ata aca cca cga aag tgc aag gct gcc gcc ctt gcc aca gcg 48
 Met Ser Ile Thr Pro Arg Lys Cys Lys Ala Ala Ala Leu Ala Thr Ala
 1 5 10 15
 ccg gtg gcc gct gcc ctc ggt gct tac gga ttt ctt aaa ggg gcg acg 96
 Pro Val Ala Ala Ala Leu Gly Ala Tyr Gly Phe Leu Lys Gly Ala Thr
 20 25 30
 aag ttc tat tcc agc cag gtt aac gga act ccc gag cag tac aag atg 144
 Lys Phe Tyr Ser Ser Gln Val Asn Gly Thr Pro Glu Gln Tyr Lys Met
 35 40 45
 acc ctt cct ggt gac gac ctc gtc ccg gaa ggt tcg ccg cgc ttc aag 192
 Thr Leu Pro Gly Asp Asp Leu Val Pro Glu Gly Ser Pro Arg Phe Lys
 50 55 60
 cgc ctc acc cat gtg gag gat ctc gac gcc ccc tgc gac gag gtc tgg 240
 Arg Leu Thr His Val Glu Asp Leu Asp Ala Pro Cys Asp Glu Val Trp
 65 70 75 80
 aag cac gtc tac cag ctc aac acc acg acc gcc ggc ttc tac tcc ttc 288
 Lys His Val Tyr Gln Leu Asn Thr Thr Thr Ala Gly Phe Tyr Ser Phe
 85 90 95
 acc ttc ttc gag aag atg ttc gga ctg tcg gtc gac aac acc ttc atg 336

Thr	Phe	Phe	Glu	Lys	Met	Phe	Gly	Leu	Ser	Val	Asp	Asn	Thr	Phe	Met		
			100					105					110				
gtg	gaa	cag	gct	tgg	cag	gcc	ccg	gac	tac	tac	aag	ccc	ggt	gac	atg	384	
Val	Glu	Gln	Ala	Trp	Gln	Ala	Pro	Asp	Tyr	Tyr	Lys	Pro	Gly	Asp	Met		
		115					120					125					
ttc	tgt	tgg	agt	tac	gcc	ggt	ttc	ggt	gcc	gag	gtc	gcc	gac	atg	gtc	432	
Phe	Cys	Trp	Ser	Tyr	Ala	Gly	Phe	Gly	Ala	Glu	Val	Ala	Asp	Met	Val		
	130					135					140						
ccc	ggc	aag	tat	ctg	gtg	tgg	ttc	gct	gac	acc	cgt	gac	ggc	acc	agg	480	
Pro	Gly	Lys	Tyr	Leu	Val	Trp	Phe	Ala	Asp	Thr	Arg	Asp	Gly	Thr	Arg		
145					150					155					160		
aca	ccg	ggc	gca	agt	ttc	ctg	cta	ccg	cct	gga	atg	ccg	tgg	aac	cgc	528	
Thr	Pro	Gly	Ala	Ser	Phe	Leu	Leu	Pro	Pro	Gly	Met	Pro	Trp	Asn	Arg		
				165					170					175			
tgg	agt	tgg	gtc	atc	gcc	ctg	gaa	ccc	ctc	gac	agt	ggc	aac	cgg	acg	576	
Trp	Ser	Trp	Val	Ile	Ala	Leu	Glu	Pro	Leu	Asp	Ser	Gly	Asn	Arg	Thr		
			180					185					190				
cgc	atc	tac	tcc	cgg	tgg	aac	atc	tcg	gcc	tcc	gag	gag	tcc	agt	ccg	624	
Arg	Ile	Tyr	Ser	Arg	Trp	Asn	Ile	Ser	Ala	Ser	Glu	Glu	Ser	Ser	Pro		
		195					200					205					
atc	tcg	gtc	ttc	ctc	atg	gat	ctg	gtc	atg	atg	gac	ggc	ggc	ggc	atg	672	
Ile	Ser	Val	Phe	Leu	Met	Asp	Leu	Val	Met	Met	Asp	Gly	Gly	Gly	Met		
		210				215					220						
gtg	aac	cgt	cgg	atg	ttc	caa	ggg	ctg	gag	aag	gct	gcc	gtc	gga	act	720	
Val	Asn	Arg	Arg	Met	Phe	Gln	Gly	Leu	Glu	Lys	Ala	Ala	Val	Gly	Thr		
225					230					235					240		
gct	cgc	aag	aac	atc	gtt	cct	gcg	cgc	cta	tca	gcg	gtt	cat	ggg	caa	768	
Ala	Arg	Lys	Asn	Ile	Val	Pro	Ala	Arg	Leu	Ser	Ala	Val	His	Gly	Gln		
				245					250					255			
gtc	cta	cgg	cac	tga												783	
Val	Leu	Arg	His														
			260														

<210> 66

<211> 260

<212> PRT

<213> Propionibacterium acnes

<400> 66

Met	Ser	Ile	Thr	Pro	Arg	Lys	Cys	Lys	Ala	Ala	Ala	Leu	Ala	Thr	Ala		
1				5					10					15			
Pro	Val	Ala	Ala	Ala	Leu	Gly	Ala	Tyr	Gly	Phe	Leu	Lys	Gly	Ala	Thr		
			20					25					30				
Lys	Phe	Tyr	Ser	Ser	Gln	Val	Asn	Gly	Thr	Pro	Glu	Gln	Tyr	Lys	Met		
		35					40					45					
Thr	Leu	Pro	Gly	Asp	Asp	Leu	Val	Pro	Glu	Gly	Ser	Pro	Arg	Phe	Lys		
	50					55					60						
Arg	Leu	Thr	His	Val	Glu	Asp	Leu	Asp	Ala	Pro	Cys	Asp	Glu	Val	Trp		
	65				70					75					80		
Lys	His	Val	Tyr	Gln	Leu	Asn	Thr	Thr	Thr	Ala	Gly	Phe	Tyr	Ser	Phe		

Thr	Phe	Phe	Glu	85	Lys	Met	Phe	Gly	Leu	90	Ser	Val	Asp	Asn	Thr	95	Phe	Met
			100						105							110		
Val	Glu	Gln	Ala	Trp	Gln	Ala	Pro	Asp	Tyr	Tyr	Lys	Pro	Gly	Asp	Met			
		115						120					125					
Phe	Cys	Trp	Ser	Tyr	Ala	Gly	Phe	Gly	Ala	Glu	Val	Ala	Asp	Met	Val			
	130					135					140							
Pro	Gly	Lys	Tyr	Leu	Val	Trp	Phe	Ala	Asp	Thr	Arg	Asp	Gly	Thr	Arg			
145					150					155					160			
Thr	Pro	Gly	Ala	Ser	Phe	Leu	Leu	Pro	Pro	Gly	Met	Pro	Trp	Asn	Arg			
				165					170					175				
Trp	Ser	Trp	Val	Ile	Ala	Leu	Glu	Pro	Leu	Asp	Ser	Gly	Asn	Arg	Thr			
			180					185					190					
Arg	Ile	Tyr	Ser	Arg	Trp	Asn	Ile	Ser	Ala	Ser	Glu	Glu	Ser	Ser	Pro			
	195					200						205						
Ile	Ser	Val	Phe	Leu	Met	Asp	Leu	Val	Met	Met	Asp	Gly	Gly	Gly	Met			
	210					215					220							
Val	Asn	Arg	Arg	Met	Phe	Gln	Gly	Leu	Glu	Lys	Ala	Ala	Val	Gly	Thr			
225					230					235					240			
Ala	Arg	Lys	Asn	Ile	Val	Pro	Ala	Arg	Leu	Ser	Ala	Val	His	Gly	Gln			
			245						250					255				
Val	Leu	Arg	His															
			260															

<210> 67
 <211> 7
 <212> DNA
 <213> Propionibacterium acnes

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<220>
 <221> RBS
 <222> (1)..(7)

<400> 67
 gaaggag

7

<210> 68
 <211> 582
 <212> DNA
 <213> Propionibacterium acnes

<220>
 <221> CDS
 <222> (1)..(582)

<400> 68																		
atg	gat	act	tca	gtc	aat	gtc	gac	acg	tcg	tca	aga	ccg	gcg	cac	gaa		48	
Met	Asp	Thr	Ser	Val	Asn	Val	Asp	Thr	Ser	Ser	Arg	Pro	Ala	His	Glu			
1				5				10					15					
ccg gcc acc gct ccc ggt cgt ttc gtc gtc aga gat gcc tgt cac gag																		96
Pro	Ala	Thr	Ala	Pro	Gly	Arg	Phe	Val	Val	Arg	Asp	Ala	Cys	His	Glu			
			20					25					30					
gac ctg cct gaa gcc gcg gct gtt cag gcc gtg tgc gtc cga gag atc																		144
Asp	Leu	Pro	Glu	Ala	Ala	Ala	Val	Gln	Ala	Val	Cys	Val	Arg	Glu	Ile			
			35				40					45						

ggc cag ggg gtg atc cct aat gac gtc ctt acc gag gtc act ggc ccc	192
Gly Gln Gly Val Ile Pro Asn Asp Val Leu Thr Glu Val Thr Gly Pro	
50 55 60	
ggt atc gtc cac acc acc att gag cag tgg aac cac ttt atg gat gat	240
Gly Ile Val His Thr Thr Ile Glu Gln Trp Asn His Phe Met Asp Asp	
65 70 75 80	
ggt gcg atc ttc aag atc ctt gtt gat cgc ctc gat atg agg act gtc	288
Gly Ala Ile Phe Lys Ile Leu Val Asp Arg Leu Asp Met Arg Thr Val	
85 90 95	
ggg gtt gcc atg gcc cgg gtc tct aca agt tct gat gct ccc aca ccg	336
Gly Val Ala Met Ala Arg Val Ser Thr Ser Ser Asp Ala Pro Thr Pro	
100 105 110	
tgg gag atc gcg acc ctc cat gta ctg cca gag gcg cga aac tgc gga	384
Trp Glu Ile Ala Thr Leu His Val Leu Pro Glu Ala Arg Asn Cys Gly	
115 120 125	
gcg tca gac aac ctc ctc gat gct tgt atc ggg aac cgg tcg gcc tat	432
Ala Ser Asp Asn Leu Leu Asp Ala Cys Ile Gly Asn Arg Ser Ala Tyr	
130 135 140	
gtg tgg gtc ttt gcc gat aat gct cgc gcc att tcg ttc tac caa cgc	480
Val Trp Val Phe Ala Asp Asn Ala Arg Ala Ile Ser Phe Tyr Gln Arg	
145 150 155 160	
cat ggg ttc cac gtc gac gcg gcc gac ggt gcc gtt gac gat tcc ctc	528
His Gly Phe His Val Asp Ala Ala Asp Gly Ala Val Asp Asp Ser Leu	
165 170 175	
ggc ggg gta gag ctg cag cgg ctg atc cgc gag gac atc atc gag tcg	576
Gly Gly Val Glu Leu Gln Arg Leu Ile Arg Glu Asp Ile Ile Glu Ser	
180 185 190	
cag tga	582
Gln	

<210> 69

<211> 193

<212> PRT

<213> Propionibacterium acnes

<400> 69

Met Asp Thr Ser Val Asn Val Asp Thr Ser Ser Arg Pro Ala His Glu	
1 5 10 15	
Pro Ala Thr Ala Pro Gly Arg Phe Val Val Arg Asp Ala Cys His Glu	
20 25 30	
Asp Leu Pro Glu Ala Ala Ala Val Gln Ala Val Cys Val Arg Glu Ile	
35 40 45	
Gly Gln Gly Val Ile Pro Asn Asp Val Leu Thr Glu Val Thr Gly Pro	
50 55 60	
Gly Ile Val His Thr Thr Ile Glu Gln Trp Asn His Phe Met Asp Asp	
65 70 75 80	
Gly Ala Ile Phe Lys Ile Leu Val Asp Arg Leu Asp Met Arg Thr Val	
85 90 95	
Gly Val Ala Met Ala Arg Val Ser Thr Ser Ser Asp Ala Pro Thr Pro	
100 105 110	
Trp Glu Ile Ala Thr Leu His Val Leu Pro Glu Ala Arg Asn Cys Gly	


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<220>  
<221> UNSURE  
<222> (1) .. (53)
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<223> Xaa = any amino acid

<400> 73

Gly Xaa Gly Xaa Xaa Gly Xaa Xaa Xaa Ala Xaa Xaa Leu Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa
20 25 30
Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
35 40 45
Xaa Xaa Xaa Xaa Gly
50

<210> 74

<211> 43

<212> PRT

<213> Homo sapiens

<400> 74

Ser Glu Ala Tyr Ser Ala Lys Ile Ala Leu Phe Gly Ala Gly Pro Ala
1 5 10 15
Ser Ile Ser Cys Ala Ser Phe Leu Ala Arg Leu Gly Tyr Ser Asp Ile
20 25 30
Thr Ile Phe Glu Lys Gln Glu Tyr Val Gly Gly
35 40

<210> 75

<211> 41

<212> PRT

<213> Agrobacterium vitis

<400> 75

Lys Val Ala Ile Val Gly Ala Gly Leu Ser Gly Leu Val Val Ala Ser
1 5 10 15
Glu Leu Leu His Ala Gly Ile Asp Asp Val Thr Leu Tyr Glu Ala Ser
20 25 30
Asp Arg Ile Gly Gly Lys Leu Trp Ser
35 40

<210> 76

<211> 45

<212> PRT

<213> Deinococcus radiodurans

<400> 76

Val Lys Thr Gly Lys Lys Val Ala Val Val Gly Ser Gly Pro Ala Gly
1 5 10 15
Leu Ala Ala Ala Gln Gln Leu Ala Arg Ala Gly His Asp Val Thr Val
20 25 30
Phe Glu Lys Asn Asp Arg Val Gly Gly Arg Ile Glu Gln

35

40

45

<210> 77

<211> 37

<212> PRT

<213> *Arthrobacter nicotinovorans*

<400> 77

Val Val Gly Gly Gly Phe Ser Gly Leu Lys Ala Ala Arg Asp Leu Thr
 1 5 10 15

Asn Ala Gly Lys Lys Val Leu Leu Leu Glu Gly Gly Glu Arg Leu Gly
 20 25 30

Gly Arg Ala Tyr Ser
 35

<210> 78

<211> 52

<212> PRT

<213> *Synechocystis* sp.

<400> 78

Arg Ile Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ala Thr Ala Val
 1 5 10 15

Glu Leu Val Asp Ala Gly His Glu Val Glu Leu Tyr Glu Ala Arg Ser
 20 25 30

Phe Ile Gly Gly Lys Val Gly Ser Trp Val Asp Gly Asp Gly Asn His
 35 40 45

Ile Glu Met Gly
 50

<210> 79

<211> 57

<212> PRT

<213> *Cercospora nicotianae*

<400> 79

Ser Thr Ser Lys Arg Pro Thr Ala Ile Val Ile Gly Ser Gly Val Gly
 1 5 10 15

Gly Val Ser Thr Ala Ala Arg Leu Ala Arg Ala Gly Phe His Val Thr
 20 25 30

Val Leu Glu Lys Asn Asn Phe Thr Gly Gly Arg Cys Ser Leu Ile His
 35 40 45

His Glu Gly Tyr Arg Phe Asp Gln Gly
 50 55

<210> 80

<211> 52

<212> PRT

<213> *Zea mays*

<400> 80

Arg Val Ile Val Val Gly Ala Gly Met Ser Gly Ile Ser Ala Ala Lys
1 5 10 15

Arg Leu Ser Glu Ala Gly Ile Thr Asp Leu Leu Ile Leu Glu Ala Thr
20 25 30

Asp His Ile Gly Gly Arg Met His Lys Thr Asn Phe Ala Gly Ile Asn
35 40 45

Val Glu Leu Gly
50

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